MRITool User's Manual

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Abstract

MRITool is a Matlab package for functional Magnetic Resonance Imaging (fMRI) reconstruction. It implements different reconstruction methods and provides a quite flexible graphical interface. The work was financed by the Italian MURST Project "Numerical Analysis: Methods and Mathematical Software" 1998–2000 (*http://www.unife.it/AnNum97*).

The software, developed by mathematicians in cooperation with other reserchers working at the Department of Nuclear Medicine of Careggi Hospital, was firstly motivated by the fact that the reconstruction method available on the Phillips MRI system at the Hospital was not completely satisfactory. In fact, it is known in literature that this method, the *Keyhole* method, can produce artifacts in the reconstructed MRI images. Our research started by investigating some alternative methods proposed in literature and the MRITool software is the mean to analyse with the medicians the results obtained. With the toolbox it is possible to test the methods on real data sets (acquired for example by the 1.5T wholebody Phillips system at the Careggi Hospital), as well as on "simulated" data.

MRITool is freely available (for non commercial use only) from the URL *http://dm.unife.it/~mritool*.

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Chapter 1

Introduction

This software was developed during the work made for the Italian MURST project "Numerical Analysis: Methods and Mathematical Software", 1998–2000 (*http://www.unife.it/AnNum97*). One of the main results obtained with this work is that an interdisciplinary collaboration between medicians, physicians, engeneers and mathematicians has started on an interesting research topic.

The problem considered concerns functional Magnetic Resonance Imaging (fMRI). The work was mainly motivated by the fact that the reconstruction method available on the commercial systems is not completely satisfactory. The aim of our work is to study alternative numerical methods for fMR images reconstruction from the acquired data in the Fourier space [1, 2, 4, 3].

The final product of our work is a Matlab software package that provides a graphical interface, some reconstruction methods alternative to the *Keyhole* and few instruments for the images visualization. The package is available from the URL *http://dm.unife.it/~mritool*. The reconstructed images can then be used for an "a posteriori" analysis that can be executed with the existing instruments and software.

The toolbox is constituted of Matlab programs and functions. We choose the Matlab environment for its easy use of numerical and graphical instruments and for its large diffusion. In the last years some software packages have been produced to create virtual graphical environments for functional neuroimages such as Positron Emission Tomography (PET or SPECT) and fMRI: *V3*, produced by the Liang's group and written in C language (*http://mri.beckman.uiuc.edu*), *Lyngby*, a Matlab fMRI analysis toolbox (*http://hendrix.imm.dtu.dk/software*) written at the Thor Center for Neuroinformatics of the Technical University of Denmark, and the fMRI analysis package by Pawel Skudlarski (*http://mri.med.yale.edu*), from the Division of Imaging Sciences Diagnostic Radiologies of the Yale University. However, while the former does not provide a graphical interface and it does not enable the use of different regularization methods, the latters perform the analysis of reconstructed images without implementing methods for the images reconstruction.

The key is that PET and fMRI probes in vivo patterns of activity in the human brain. Anything short of an interactive real-time display will not fully be able to represent the richness of these spatio-temporal phenomena. Virtual environments play a fundamental role in mediating the dialogue between medicians, engineers and physicists.

Further details and deeper treatement of the subject, together with a larger bibliography, can be found in [5].

Chapter 2

Installation and getting started

The only software resource necessary to use MRITool is the Matlab package, version 5.2 or higher. At present, MRITool has been tested on Unix systems (Dec-ALPHA based and SUN) and on Windows platform (WindowsNT, Windows95 and Windows98). The source files are the same for all the platforms (compressed in different forms for the different systems), while the data files for demos are different, because they are stored in binary format (Matlab files with extension " .mat"). The software is available at the URL *http://dm.unife.it/~mritool*. The installation procedure is the following:

Unix systems. Move to your favourite directory or to the Matlab's *toolbox* directory, download the source tar file `mritool_src.tar.gz` and give the following commands at the line prompt:

```
gunzip mritool_src.tar.gz
tar xvf mritool_src.tar
```

These will expand the MRITool directory tree as a child (called *mritool*) of the current directory. If you want the demo data, from the same directory download also the data file `mritool_data.tar.gz` and repeat on this file the previous commands:

```
gunzip mritool_data.tar.gz
tar xvf mritool_data.tar
```

These commands will add the MAT-files in the *files/input* subdirectory of the *mritool* tree. Note that if you have `gtar` (GNU `tar`) installed, you can replace the two commands `gunzip` and `tar xvf` with the `gtar xvzf` command.
Now you can remove the `.tar` files from your directory. If you are performing a multiuser installation, remember to adjust the permissions of the directory tree.

Windows systems. Download the compressed source file `mritool_src.zip` and uncompress it with WinZip® or another suitable program, using as destination your favorite folder or the *toolbox* folder of your Matlab tree.

After these operations you have a new subdirectory called *mritool* that contains all the toolbox files. By the same way, if you want the demo data, download the `mritool_data.zip` file and repeat the uncompressing operation, unsing this time as destination the subfolder *files\input* of the existing *mritool* folder.

Start Matlab and add *mritool* to your Matlab path: use the path browser or your `startup.m` file if you want to add it permanently, or use the command `path` from the command window if you want to add it only temporarily. In the last case, you can first move to the MRITool parent directory ad give the command

```
>> path(path,fullfile(pwd,'mritool',''));
```

or use the `path` command with the absolute *mritool* path from everywhere:

```
>> path(path,fullfile(matlabpath,'toolbox','mritool',''));
```

(see the Matlab Reference manual or the on-line help for a description of the `fullfile` command). Remember that in this case you will have to repeat the procedure for any new Matlab session.
Now you are ready to use MRITool by giving the command

```
>> mritool
```

in the Matlab's command window. This will open the graphical interface in a full screen style, leaving the command window still opened in background so you will be able to perform further computation during your MRITool session. All the MRITool functionalities are available from pup-up menus and you do not need to type anything at the command line.

A brief description of all the commands is provided in the form of comments, through the help system in the command window, as described in the next section, so you could also directly call the tool scripts and functions from the Matlab prompt. However, since in this first release we still make a rather wide use of global variables, many functions need some variables and/or arrays already defined in the Matlab global workspace and it can be difficult to use the functions independently from the prompt.

2.1 Getting help

MRITool help can be viewed from the graphical interface, by clicking the **Help** button or by choosing the **Help** option from the main menu bar: this will show you the main help window through the default hypertext browser of your system, that you can use to read all the functions description. If you have not a default browser configured on your system, the standard Matlab help GUI will be opened.

From the Matlab command window, you can get help for each function from the Matlab prompt. For example, if you want to get help for the `keyhole` function, you just need to type

```
>> help keyhole
```

as usual in Matlab. This version does not provide the same level of detail for all the scripts and functions, so you could experience difficulties in some cases. This will be fixed in a next release, however all the reconstruction codes are based on the theory described in this work.

Chapter 3

MRITool overview

This toolbox provides some methods for the reconstruction of a sequence of fMRI images from the acquired data and some tools for the visualization of the reconstructed images. Briefly, the steps for the reconstruction of a fMRI sequence of images are:

1. choose a data set or retrieve the data saved from a previous session;
2. choose the method for the images reconstruction;
3. choose the sections to be visualized; After the reconstruction, you are allowed to choose, in any order, which and how many sections will be displayed and the 2D grid in which the images will appear. Once all the images are displayed on the screen, you are allowed to move or resize them. You can perform a set of visualization operations on the figures all at once, as described in section 4.5. Furthermore, each image can also be independently elaborated.

When you want to leave the tool or to change the data, you will have to

1. save the session with if you want to continue your job later;
2. close the images on the screen;
3. leave the tool.

With this version it is possible to reconstruct:

(a) a sequence of dynamic MRI images from available real data;

(b) a sequence of dynamic MRI images from your own data, acquired in the frequency-phase space and preprocessed to meet the required input format (see the description in section 4.1 and the example file `read_binary.m` in the *mritool* directory).

The method for the images reconstruction can be chosen between the following:

- Reduced-encoding Imaging by Generalized-series Reconstruction with one reference image (RIGR1).
- Reduced-encoding Imaging by Generalized-series Reconstruction with two reference images (RIGR2).

- Keyhole.

The methods RIGR1 and RIGR2 are combined with regularization methods for the solution of ill–conditioned linear systems. For each regularization method, some choices for the automatic computation of the regularization parameter are proposed, together with a custom setting.

Furthermore, it is possible to show or hide the figure's toolbar, by which you can access many other standard useful commands as saving or exporting the image on an external file, printing, zooming, etc. (refere to the Matlab manual or to the on-line help for more information).

Chapter 4

Using the MRITool graphical interface

MRITool provides a graphical interface based on the powerful Matlab GUI system [10, 7]. It consists of three main parts:

- a full screen frame that constitutes a workbanch for the visualization and elaboration of the reconstructed images;
- a main menu bar at the top of the screen, which gives access to all the available functionalities of the tool as weel as to the help system;
- a set of five push buttons at the bottom of the screen, to facilitate the use of the tool to beginners. In fact, The functions called by the five buttons are essentially the same as those called by the menu items, but the push buttons use a more friendly approach through successive GUI windows, each having its own help button to briefly explain some details of the related reconstruction step.

Some examples of the graphical interface during a work session is given in figures 4.1, 4.14 and 4.15. It can be noticed that buttons and menus are automatically enabled/disabled depending on the current state of your work.

In the following subsections we'll give an overview of the main features available through the main menu items.

4.1 Load option

The **Load** menu loads a data set to be processed. There are some demo data sets already available from the MRITool web site as MAT-files for different platforms, but the user can process its own data, once they are provided as MAT-files in the correct format. This is obtained by using a suitable function that reads the raw data acquired by the MRI device and then converts them in a 3D array: we give below a brief description of this preprocess and we refer the reader to the self explaining function `read_binary.m` for a more detailed description.

The available demo data are of two types (Fig. 4.2) and they are both acquired from a 1.5T wholebody MR Phillips system:

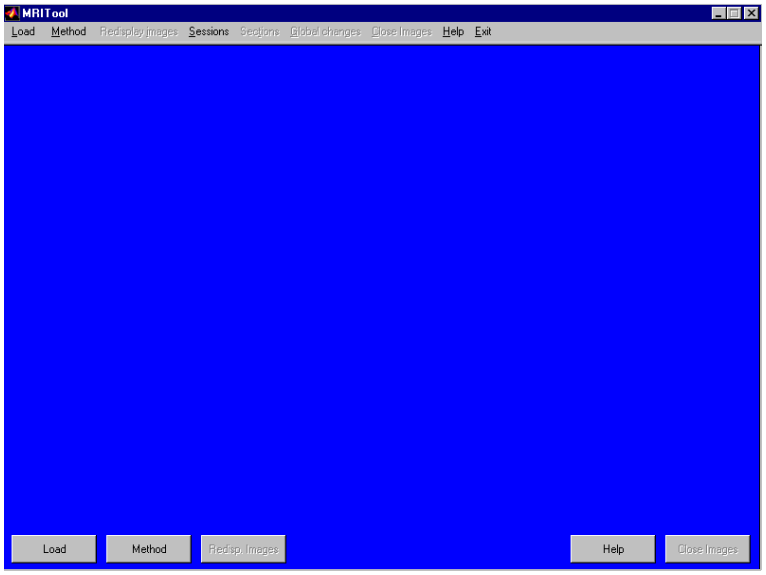

Figure 4.1: The basic MRITool graphical interface.

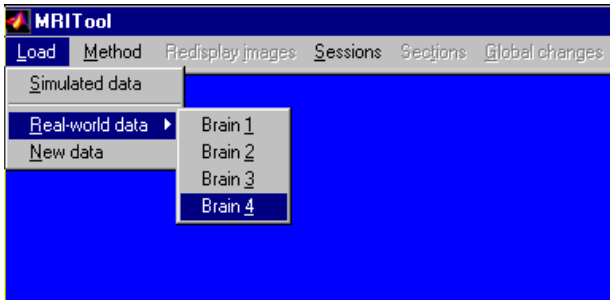

Figure 4.2: The **Load** menu from the main menu bar.

- the **Simulated data** item loads data constituted of one reference set and one dynamic set, each of 256×256 samples. By considering only a reduced set of phase samples (32 phases) from the dynamic set, we simulate the undersampling process of the MRI system. As an exception, these data are contained in two ASCII files;

- the **Real-world data** item loads four sequences of data: Brain 1, Brain 2, Brain 3, Brain 4. They all are related to the same patient and each one has the following characteristics:

  - KeyHole: 20%
  - RFOV: 70%
  - Scan percentage: 80%
  - Scan matrix: 128
  - Reconstruction matrix: 256
  - Two reference sets of 128×70 samples (section numbers 1 and 59);
  - 57 dynamic sets of 128×19 samples (section numbers 2–58).

Finally, with the **New data** option (Fig. 4.3) it is possible to process other data sets. As mentioned, a preprocessing computation must be done in order to create appropriate MAT-files necessary for the reconstruction with MRITool: two of them are required, i.e. the one for the initial (baseline) reference data set and the one for the dynamic sets; the third file, for the final (active) reference set, can be omitted and in this case you will have not access to RIGR2 reconstruction methods. The format for the contents of the three files is the following:

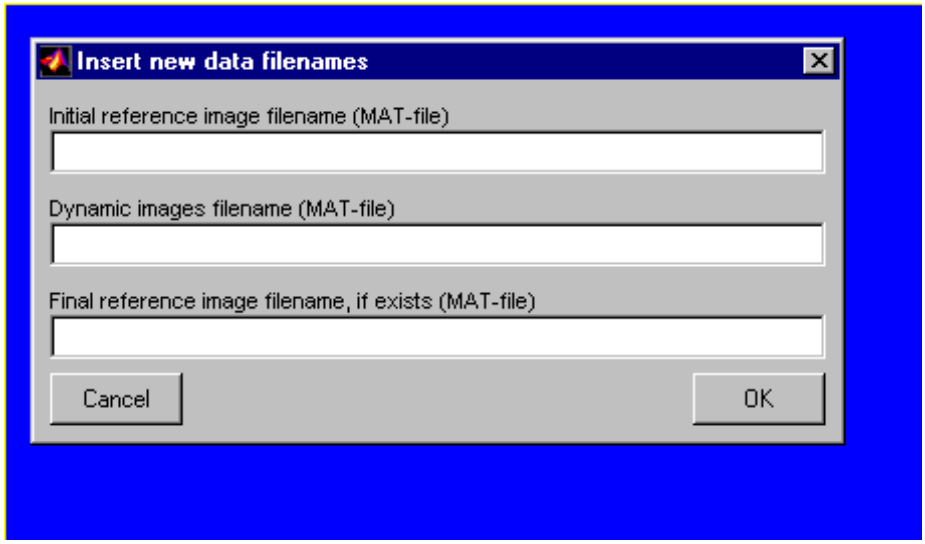

Figure 4.3: The window appearing for the loading of new data.

Initial reference image: this file must contain the baseline reference data set. It must be stored in a matrix of size $N \times M$, where N is the number of frequency samples and M is the number of phase samples.

Dynamic images: this file must contain the dynamic data acquired at time instants $t_1, \ldots, t_Q$. The data must be stored in a $N \times N_m \times Q$ array, where N is the number of frequency samples and N_m is the reduced number of phase samples acquiresd at each time instant t_j, $j = 1, \ldots, Q$.

Final reference image: this file, if present, must contain the active reference data set. It must be stored in a matrix of size $N \times M$, where N is the number of frequency samples and M is the number of phase samples.

4.2 Method option

With the **Method** menu you can choose a reconstruction method for the sequence of fMRI images. The available choices are the following:

1. **Keyhole**: loads the Keyhole method [5, section 1.4];
2. **RIGR One Ref.**:loads the Reduced-encoding Imaging by Generalized series Reconstruction method with one reference image [5, section 1.5];

3. **RIGR Two Refs.**: loads the RIGR method with two reference images [5, section 1.6].

Both the RIGR1 and the RIGR2 methods require a regularization method for the solution of the hermitian and positive semidefinite linear systems, as described in section [5, section 1.7].

In this version of the tool, three regularization methods are implemented, each one having a set of rules for the choice of the "optimal" regularization parameter:

1. **TSVD** (Fig. 4.4) starts the truncated singular values decomposition method for regularization. The possible choices for the computation of the regularization parameter are:

   - **GCV**: generalized cross validation method [9]. This method is quite accurate but it needs long time for the execution;
   - **Customize**: you introduce a regularization parameter by typing a custom value. The value must be an integer in the interval $[1, N_m]$, where N_m is the number of acquired phase samples for the dynamic sets. The default value is N_m.

   We plan to add the L–curve criterion for this method in the next release.

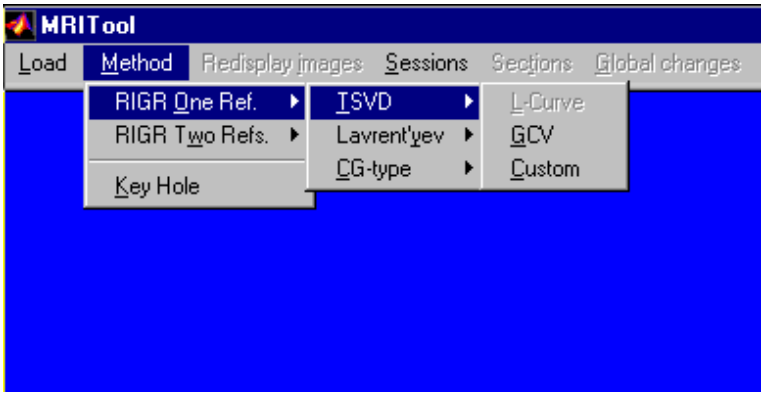

Figure 4.4: The **TSVD** menu from the menu bar.

2. **Lavrent'yev** (Fig. 4.5) starts the Lavrent'yev regularization method. The related regularization parameter can be computed by using one of the following approaches:

   - **L-Curve**: it uses the L–curve method [6, 8] which is quite accurate, but it needs long time for the execution;
   - **GCV**: it uses the generalized cross validation method;
   - **Customize**: you introduce a regularization parameter by typing a custom value. The value must be a positive number: the default is 0.1.

3. **CG-type** starts one of the four implemented conjugate gradient type regularization methods described in [5, section 1.7] (Fig. 4.6):

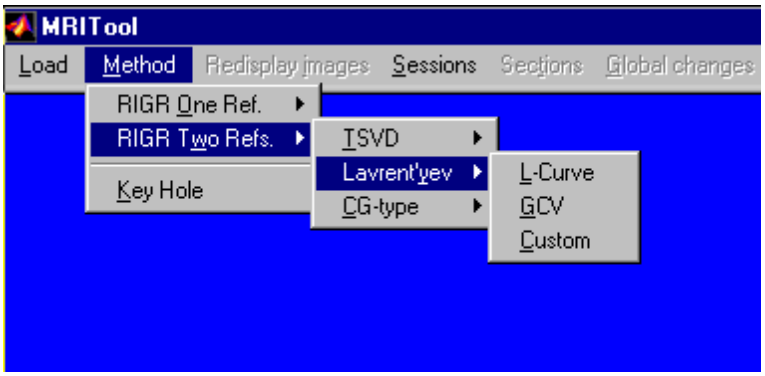

Figure 4.5: The **Lavrent'yev** menu from the menu bar.

(a) **CG** is the standard conjugate gradient method applied to the linear system;

(b) **MR** is the minimum residual method applied to the linear system;

(c) **CGNE** is the conjugate gradient method applied to the standard normal equations;

(d) **CGME** is the minimum residual method applied to the normal equations of the second kind.

For each of the CG-type methods four rules for the computation of the regularization parameter are available (stopping rules in this case):

- **Heuristic 1**: is a criterion proposed by Hanke, based on the behaviour of the Ritz polynomials (one of the rules R1, R2, R3, R4 in [5, section 1.7]);
- **Heuristic 2**: heuristic criterion based on the residuals behaviour (rule R5 in [5, section 1.7]);
- **Heuristic 3**: heuristic criterion based on the residuals behaviour (rule R6 in [5, section 1.7]);
- **Customize**: you introduce a regularization parameter by typing a custom value. The value must be a positive number in the interval $[1, N_m]$, where N_m is the number of phase samples acquired for the dynamic images. The default value is 5.

4.3 Sessions option

With this item you can save your work during a MRITool session and reload it when necessary. When at least one work session is saved (as a MAT-file), you can load or delete the related file. The available submenu are (Fig.4.7):

1. **Save**: it allows to save in a MAT-file the main MRITool variables, arrays and structures from the Matlab workspace, in order to restart later from *the same* situation. A mask appears where you can type the filename;

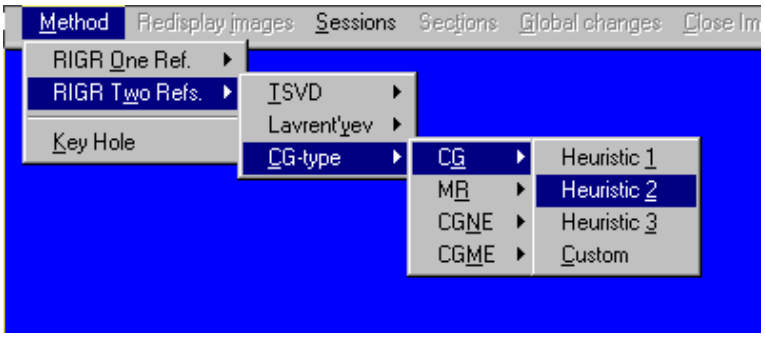

Figure 4.6: The conjugate gradient type menu from the menu bar.

2. **Load**: it loads in the Matlab workspace a previously saved work session. The current Matlab workspace is substituted by the loaded workspace and the saved state is completely retrieved (Fig. 4.8);

3. **Delete**: it allows the deletion of a previously saved file.

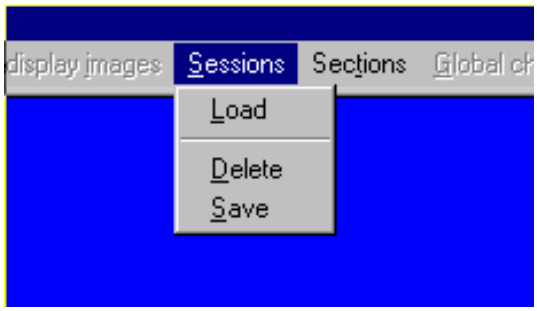

Figure 4.7: The **Sessions** menu from the menu bar.

4.4 Sections option

From this menu item a mask appears as in Fig. 4.9, containing a 2D grid that shows you how many images can be represented on the screen and how they can be positioned. The number of images that can be displayed depends on the screen resolution as well as on the image size. You can select with the mouse how many images you want to view, then a new mask appears (Fig. 4.10) where you can choose, by clicking with the mouse, which sections you want to be displayed (each section is identified by the number of its position in the sequence).With the **OK** button the visualization process starts; it can take a little, expecially if you have an high resolution screen and you select a large number of sections to display, or if you are working on a remote system.

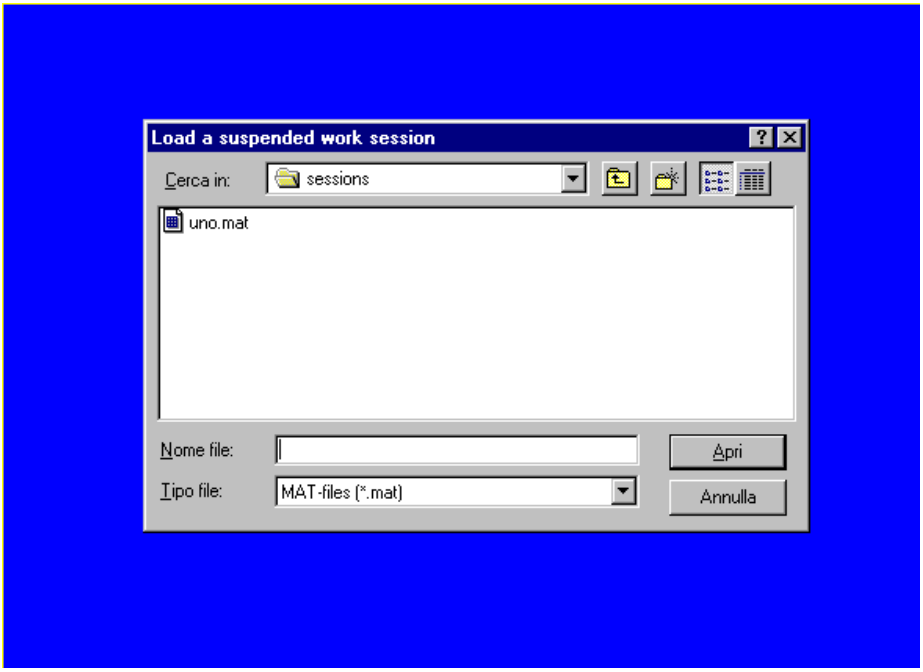

Figure 4.8: The window for loading a previously saved work session.

4.5 Global changes option

Through menu allows you to control the visualization properties of all the images on the screen. Available submenus are:

1. **Image Menubar**: switch on/off the figure's menubar;
2. **Colormap**: changes the colormap (Fig. 4.11). In this release only standard colormaps are available;
3. **Sort Images**: allows the sorting in ascending/descending order with respect to the section number, together with a "last-operation" undo (Fig. 4.13);
4. **Reset to default**: restore the default situation by redisplaying the images in their initial state. Menubars and visualization mode are taken from the current setting;
5. **Visualization mode**: this property affects the images aspect with respect to axis scaling and figure size. Available choices are:
   - **Maintain the aspect ratio**: the images are displayed by keeping the proprtion between horizontal and veritcal size as in the corresponding matrix;
   - **Fill all figure windows**: the images are displayed filling all the available figure's area. In this case the appareance can be distorted, but the zoom capabilities (available from the figure's menubar) are improved;

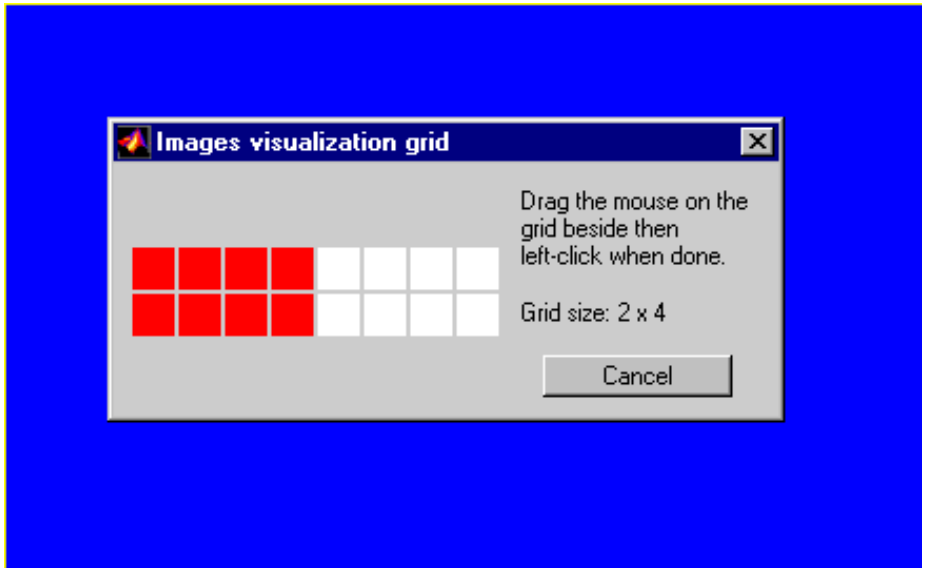

Figure 4.9: The mask appearing when choosing the **Sections** menu from the menu bar.

6. **RIGR2 images**: this submenu is available *only* for RIGR2 recontructions and allows you to choose from the following items:

   - **Show the difference images**: the images representing the changes from the baseline to the dynamic data are displayed;
   - **Show the completed images**: the dynamic images are displayed.

Each image can even be independently modified. By clicking with the right mouse button while the pointer is on the single image, the just described submenu appears so that the corresponding actions can be now performed on the single image (Fig. 4.12). However, some other items appear in this context menu:

- **Dyn. Sec.**: shows the current image section number in the whole sequence;
- **Image Size**: gives information about the displayed matrix;
- **Section**: allows you to change the displayed section;
- **History**: shows which reconstruction process was used for the current image.

4.6 Redisplay images option

This option acts by refreshing the graphical interface: it firstly recall the MRI-Tool background frame and then flush all the open figures on foreground.

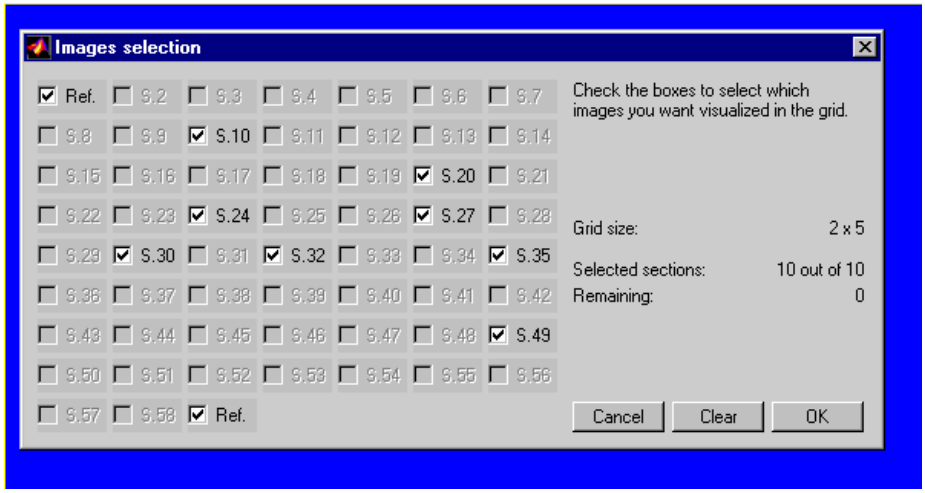
Images selection
Ref. S.2 S.3 S.4 S.5 S.6 S.7
S.8 S.9 S.10 S.11 S.12 S.13 S.14
S.15 S.16 S.17 S.18 S.19 S.20 S.21
S.22 S.23 S.24 S.25 S.26 S.27 S.28
S.29 S.30 S.31 S.32 S.33 S.34 S.35
S.36 S.37 S.38 S.39 S.40 S.41 S.42
S.43 S.44 S.45 S.46 S.47 S.48 S.49
S.50 S.51 S.52 S.53 S.54 S.55 S.56
S.57 S.58 Ref.
Check the boxes to select which images you want visualized in the grid.
Grid size: 2 x 5
Selected sections: 10 out of 10
Remaining: 0
Cancel
Clear
OK

Figure 4.10: The grid for the choice of the sections.

4.7 Close images option

It closes the displayed images, but does not leave the tool. You can still access the reconstructed images by choosing the **Sections** menu to redisplay them.

4.8 Exit option

Exit from MRITool. The Matlab workspace is cleared from the tool variables, arrays and structures, but any other "entity" is left in place, so you will not miss your own variables and computation results, apart from unfortunate name matching.

4.9 A typical reconstruction session

We test on the **Brain 1** sequence the RIGR2 method associated with the CG regularization method stopped with **Heuristic 1** criterion (see [5, section 1.7]). The reconstruction session can proceed as follows:

1. load the **Brain 1** data set with the **Load** button or menu, as in Fig. 4.2;
2. choose the **RIGR Two Refs.** reconstruction method from the **Method** menu;
3. go through the **CG-type** option and the **CG** regularization method up to the **Heuristic 1** criterion option, as in Fig. 4.6;
4. when the reconstruction is completed, select the sections to be displayed on the screen with the **Sections** menu, using the two masks of figg. 4.9 and 4.10. The selected sections are displayed with the default settings (Fig. 4.14);

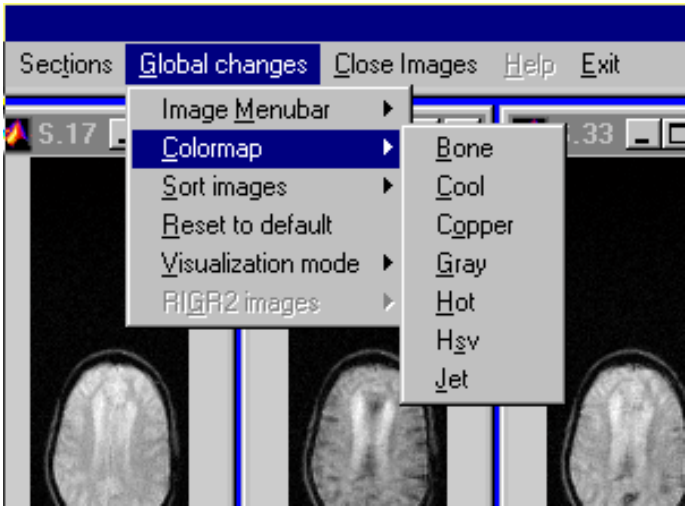

Figure 4.11: A possible choice from the **Global changes** menu: the available colormaps.

5. you can now change some properties of all the figures with one of the **Global changes** menu options. For example, in Fig. 4.15 the colormap is globally changed to **hot**.

   Otherwise, you can act on the single image by changing its size and/or its properties with the figure's menubar or with the context menus, obtained by clicking with the right mouse button while the pointer is on the image. As an example, in Fig. 4.16 some characteristics of the section 32 was modified, the figure's **Menubar** was added and a zoom was performed. With the **Export** option from the figure's **File** menu you can save the image in one of the standard graphic formats provided by Matlab.

   Moreover, from the Matlab command window you can even perform any type of computation on the reconstructed images, by accessing them in the `images` structure in the Matlab global workspace, as described in the MRITool help. However, given the complexity of the tool code, we discourage this practice and we strongly recommend that you make your computation on a copy of that structure.

6. You can finally save the current status of your work session with the **Save** option of the **Sessions** menu;

7. you can now close the figures with the **Close** menu (or the corresponding push button), without leaving the tool. At this stage, you can still make a copy of the `images` structure for your own computations;

8. now you can try a different reconstruction method on the same data with the **Method** menu (or push button), or you can load a different data set with the **Load** menu (or push button).

9. When you have done, you will exit MRITool with the **Exit** option.

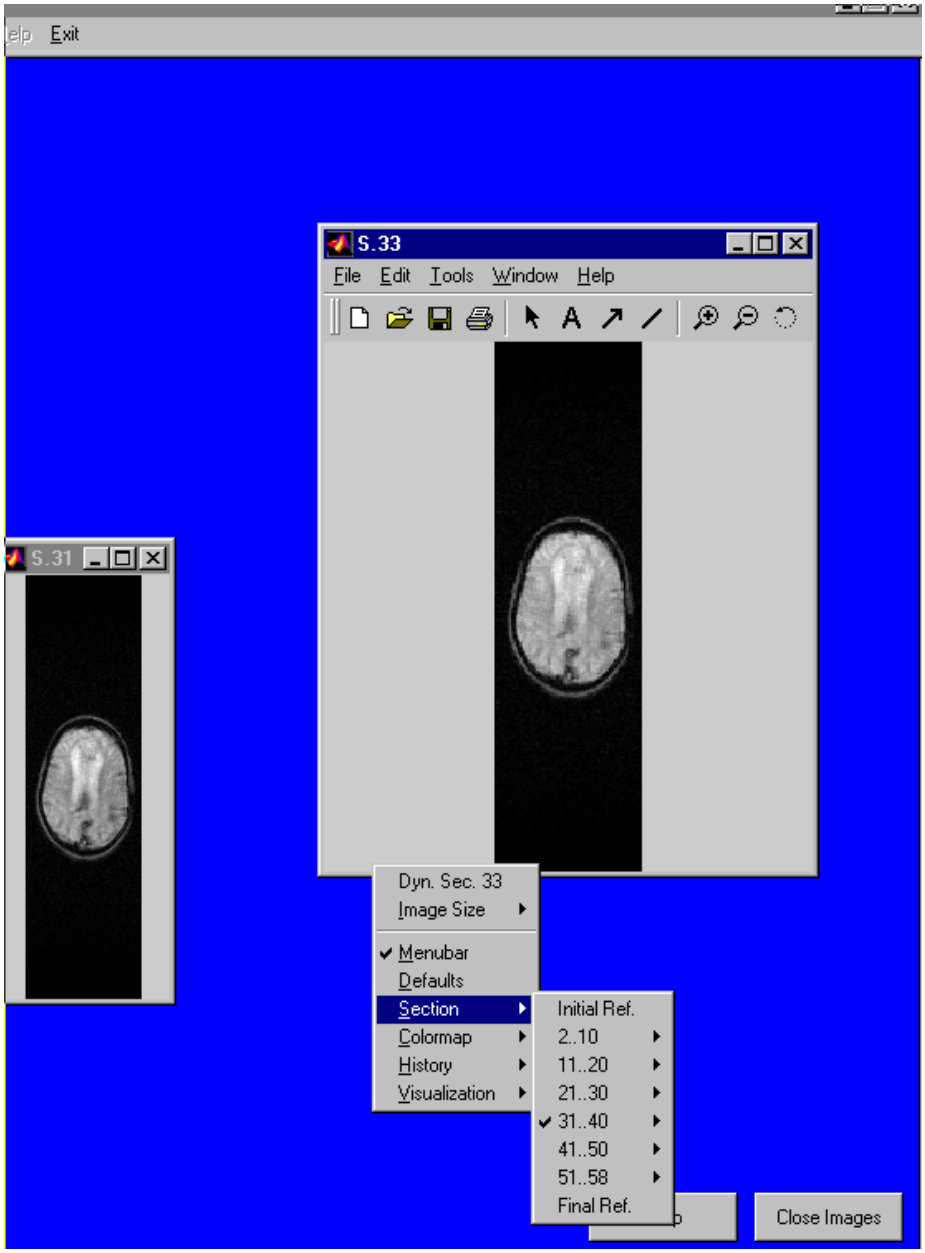

Figure 4.12: The context menu available for a single image: the **Menubar** option is "ON" for that image.

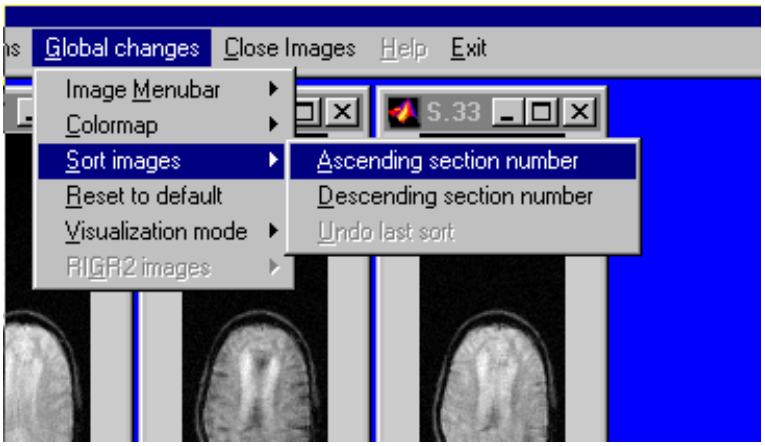

Figure 4.13: A possible choice from the **Global changes** menu: the ordering of the sections displayed on the screen with respect to their number.

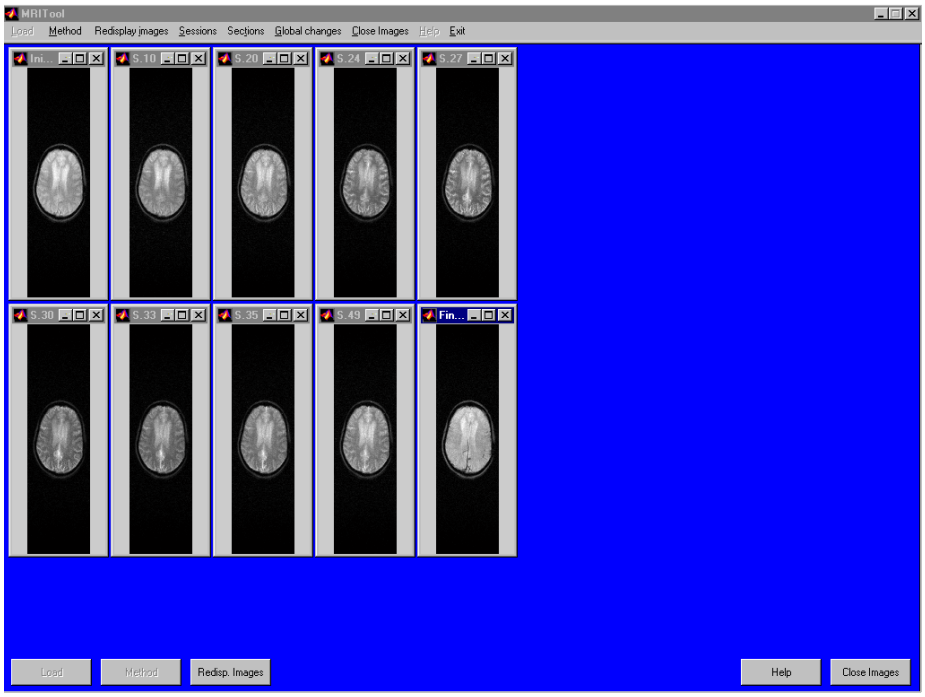

Figure 4.14: The selected sections are displayed with the default settings.

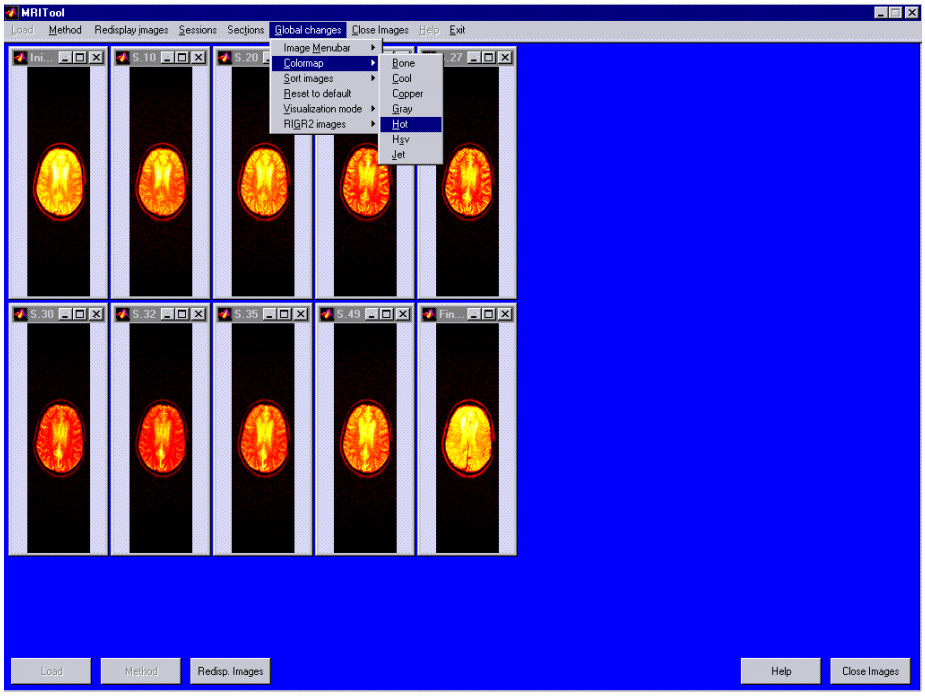

Figure 4.15: The colormap has been changed to **hot**.

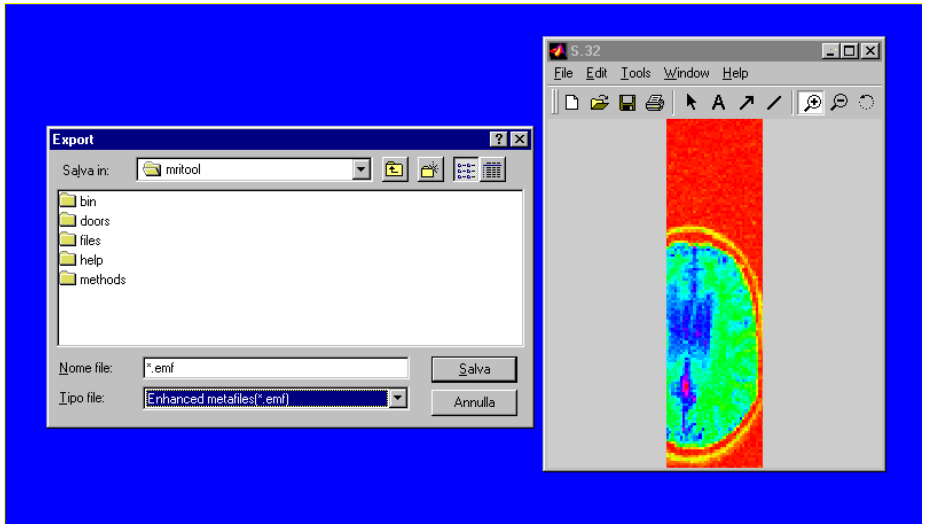

Figure 4.16: Section 32 with some characteristics modified.

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